Page 9, replace the paragraph between lines 15 – 29 with the following:

The design of methylation specific primers may be carried out using software such as "Primo MSP 3.4." It is preferred that the design of methylation specific primers be carried out according to the following guidelines:

- Primers should contain at least one CpG site within their sequence, and the CpG site should preferably be located in the most 3'-end of their sequence to discriminate methylated DNA against unmethylated DNA.
- Primers should have a minimal number of non-CpG cytosines in their sequence to amplify only bisulfite converted DNA. Primers with more non-CpG cytosines are preferred, since the bisulfite conversion may on some occasions be incomplete.
- The set of primers for methylated DNA and the set for unmethylated DNA should contain the same CpG sites within their sequence. For example, if a forward primer for methylated DNA has this sequence: ATTAGTTTCGTTTAAGGTTCGA (SEQ ID NO:15), the forward primer for unmethylated DNA must also contain the two CpG sites as the methylated forward primer. However, they may differ in length and start position.
- Both sets of primers should have similar annealing temperature.

Page 17, replace the paragraph between lines 1 – 8 with the following:

The corresponding reference assay was performed using the following primers ~~and probes~~:Primer: TCCATATTCCAAACCCTATACCAAA (SEQ ID NO:13);Primer: TGGGATTGAGGGTAAGAGGGAT (SEQ ID NO:14). The reaction is run with the following assay conditions:*Reaction solution*: (900 nM primers; 300 nM probe; 3.5 mM Magnesium Chloride; 1 unit of taq polymerase; 200 $\mu$M dNTPs; 7$\mu$l of DNA, in a final reaction